2/2021

Daytime napping (Dashti, 2021)

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Nature Communications

Behavior | Sleep

Daytime napping has some health benefits but has also been linked to certain health risks.

STUDY SUMMARY

Discovery of 123 regions of the genome associated with daytime napping.

YOUR RESULT

4th
PERCENTILE
Very low genetic predisposition to **daytime napping**

STUDY DESCRIPTION

Nearly one-third of individuals in the United States typically take a nap every day. In other parts of the world, such as in the Mediterranean, napping is even more common. While napping can greatly help improve alertness and memory, a midday snooze is also believed to affect physical health. Genetic factors appear to have a big influence on whether an individual takes regular naps or not. For example, a study of identical twins found the heritability of napping to be 65%. This genome-wide association study examined nearly 1 million individuals of European ancestry and found 123 variants associated with the tendency to take daytime naps. Among the identified genes were multiple that have previously been linked to sleep disorders (e.g. HCRTR1 And HCRTR2). Interestingly, the results of the study also pointed to a potential connection between napping and higher blood pressure, as well as larger waist circumference.

DID YOU KNOW?

Studies have suggested that an afternoon nap may be more effective than a cup of coffee at improving focus and increasing alertness.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to daytime napping we summed up the effects of genetic variants that were linked to daytime napping in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to daytime napping. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to daytime napping. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to daytime napping. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for daytime napping to be 0.73**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for daytime napping is in the **4th percentile**. This means that it is higher than the polygenic scores 4% of people. We consider this to be a **very low genetic predisposition to daytime napping**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our Nebula Library tutorial.

VARIANT	YOUR GENOTYPE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs11615756_T	C / C	0.02 (-)	31%	1.92×10^{-87}
rs385199_A	C / C	0.02 (-)	87%	1.36×10^{-72}
rs2431108_C	T / T	0.01 (-)	24%	9.95×10^{-68}
rs2653349_A	G / G	0.02 (-)	16%	5.87×10^{-62}
rs9965170_G	G / G	0.01 (↑)	64%	1.54×10^{-44}
rs13284688_C	T / C	0.01 (↑)	18%	1.33×10^{-43}
rs12140153_G	G / G	0.02 (↑)	94%	6.97×10^{-41}
rs2250377_A	A / G	0.01 (↑)	28%	7.20×10^{-40}
rs2861805_A	A / A	0.01 (↑)	73%	2.50×10^{-28}
rs10875622_A	A / A	0.01 (↑)	57%	6.24×10^{-26}
rs174541_C	T / T	0.01 (-)	31%	1.94×10^{-23}
rs11258652_C	C / C	0.01 (↑)	80%	4.05×10^{-23}
rs1001817_C	C / T	0.01 (↑)	49%	1.79×10^{-22}
rs12451365_C	T / T	0.01 (-)	34%	5.00×10^{-22}
rs13033444_G	A / G	0.01 (↑)	22%	4.01×10^{-20}
rs2769916_A	G / A	0.01 (↑)	72%	1.04×10^{-19}
rs6919087_T	T / T	0.01 (↑)	71%	1.48×10^{-18}
rs542011541_CT	NA	0.01 (-)	1%	2.17×10^{-18}
rs11967137_A	A / G	0.01 (↑)	80%	2.93×10^{-18}
rs271057_C	C / T	0.01 (↑)	35%	5.45×10^{-18}
rs224111_G	G / A	0.01 (↑)	61%	1.62×10^{-17}
rs3935190_A	G / A	0.01 (↑)	52%	3.37×10^{-17}
rs1592544_C	C / T	0.01 (↑)	53%	6.04×10^{-17}
rs962247_G	G / A	0.01 (↑)	57%	1.45×10^{-16}
rs9998136_G	C / G	0.01 (↑)	69%	1.49×10^{-16}
rs4983329_A	A / C	0.01 (↑)	54%	6.28×10^{-16}
rs35039375_G	A / A	0.01 (-)	7%	2.09×10^{-15}
rs13023587_C	C / G	0.01 (↑)	47%	2.12×10^{-15}
rs350785_T	T / T	0.01 (↑)	10%	2.29×10^{-15}
rs80163246_C	T / T	0.01 (-)	8%	3.53×10^{-15}
rs60222088_C	C / C	0.01 (↑)	80%	1.15×10^{-14}
rs10149986_G	T / G	0.01 (↑)	18%	1.15×10^{-14}
rs34728579_C	T / T	0.01 (-)	22%	1.22×10^{-14}
rs17265513_C	T / T	0.01 (-)	16%	1.44×10^{-14}
rs2786547_C	C / T	0.01 (↑)	85%	1.76×10^{-14}
rs10875606_C	A / A	0.01 (-)	36%	2.11×10^{-14}
rs35011311_G	G / G	0.01 (↑)	81%	2.50×10^{-14}
rs9883093_G	T / G	0.01 (↑)	55%	2.63×10^{-14}

rs2195272_T	G / G	0.01 (-)	29%	2.67×10^{-14}
rs971415_A	A / A	0.01 (↑)	87%	1.23×10^{-13}
rs4604518_G	G / A	0.01 (↑)	49%	2.06×10^{-13}
rs17158413_A	G / A	0.01 (↑)	21%	2.13×10^{-13}
rs13263535_G	T / T	0.01 (-)	99%	2.87×10^{-13}
rs11224896_T	T / T	0.01 (↑)	95%	3.96×10^{-13}
rs1931175_G	C / C	0.01 (-)	30%	5.41×10^{-13}
rs301817_A	A / A	0.01 (↑)	63%	5.76×10^{-13}
rs113493369_C	NA	0.01 (-)	1%	7.54×10^{-13}
rs3810484_A	A / G	0.01 (↑)	52%	1.31×10^{-12}
rs528301822_T	A / A	0.01 (-)	27%	1.35×10^{-12}
rs10257273_A	A / A	0.01 (↑)	69%	1.38×10^{-12}
rs351776_C	A / A	0.01 (-)	43%	2.21×10^{-12}
rs113960908_GGT	G / GGT	0.01 (↑)	15%	2.49×10^{-12}
rs7422655_C	T / T	0.01 (-)	37%	3.02×10^{-12}
rs12346996_T	T / C	0.01 (↑)	21%	3.74×10^{-12}
rs3732085_C	C / C	0.01 (↑)	70%	3.87×10^{-12}
rs285815_T	A / A	0.01 (-)	37%	5.11×10^{-12}
rs77154532_A	A / A	0.01 (↑)	67%	5.40×10^{-12}
rs140506252_A	A / A	0.02 (↑)	99%	5.76×10^{-12}
rs9460110_C	T / T	0.01 (-)	25%	9.09×10^{-12}
rs2099810_A	A / G	0.01 (↑)	61%	1.53×10^{-11}
rs1941182_A	C / C	0.01 (-)	34%	2.06×10^{-11}
rs141957346_AT	NA	0.01 (-)	1%	3.48×10^{-11}
rs1883048_C	T / T	0.01 (-)	50%	3.81×10^{-11}
rs35127490_CG	NA	0.01 (-)	1%	4.55×10^{-11}
rs9309116_T	C / T	0.01 (↑)	66%	5.25×10^{-11}
rs4236060_T	C / T	0.01 (↑)	23%	5.34×10^{-11}
rs35851551_A	A / A	0.01 (↑)	94%	5.61×10^{-11}
rs11125776_T	T / T	0.01 (↑)	85%	1.09×10^{-10}
rs4356873_C	T / C	0.01 (↑)	32%	1.37×10^{-10}
rs910187_G	G / A	0.01 (↑)	73%	2.56×10^{-10}
rs1415218_T	C / C	0.01 (-)	29%	2.57×10^{-10}
rs9389556_G	C / C	0.01 (-)	26%	2.97×10^{-10}
rs62560863_T	C / C	0.01 (-)	10%	3.26×10^{-10}
rs10835420_T	A / A	0.01 (-)	87%	4.12×10^{-10}
rs12614085_C	T / T	0.01 (-)	8%	4.41×10^{-10}
rs17049683_G	A / G	0.01 (↑)	31%	6.73×10^{-10}
rs62189006_A	A / A	0.01 (↑)	92%	6.85×10^{-10}
rs2370926_T	T / C	0.01 (↑)	70%	7.31×10^{-10}
rs10811438_G	C / C	0.01 (-)	63%	7.68×10^{-10}
rs2699869_A	C / C	0.01 (-)	44%	1.01×10^{-9}
rs60920123_G	G / A	0.01 (↑)	61%	1.77×10^{-9}
rs4357022_G	T / G	0.01 (↑)	50%	1.91×10^{-9}
rs9939355_C	T / T	0.01 (-)	52%	2.14×10^{-9}
rs7814873_C	T / T	0.01 (-)	31%	2.26×10^{-9}
rs2417268_T	A / A	0.01 (-)	45%	5.05×10^{-9}
rs3943782_G	A / A	0.01 (-)	27%	5.93×10^{-9}
rs112520848_C	G / G	0.01 (-)	36%	7.09×10^{-9}
rs388016_A	A / G	0.01 (↑)	63%	7.14×10^{-9}
rs2836909_G	A / A	0.01 (-)	29%	9.13×10^{-9}
rs2893323_A	G / G	0.01 (-)	29%	1.07×10^{-8}
rs6663012_T	G / G	0.01 (-)	99%	1.18×10^{-8}
rs1518394_G	G / G	0.00 (↑)	68%	1.28×10^{-8}
rs936944_G	A / A	0.01 (-)	13%	1.29×10^{-8}
rs17502738_T	C / C	0.01 (-)	85%	1.41×10^{-8}
rs76824303_A	A / A	0.01 (↑)	85%	3.59×10^{-8}
rs1843815_T	A / A	0.00 (-)	43%	5.92×10^{-8}
rs2284015_G	C / G	0.01 (↑)	30%	9.38×10^{-8}
rs10152428_C	NA	0.01 (-)	1%	1.10×10^{-7}
rs34262487_C	C / C	0.01 (↑)	99%	1.12×10^{-7}

rs253666_A	A / A	0.01 (↑)	81%	2.73×10^{-7}
rs12031519_A	A / A	0.01 (↑)	90%	3.44×10^{-7}
rs4692709_C	T / T	0.00 (–)	49%	3.83×10^{-7}
rs12657723_T	T / T	0.00 (↑)	27%	6.41×10^{-7}
rs11071755_G	G / G	0.00 (↑)	74%	7.53×10^{-7}
rs56180058_C	T / T	0.01 (–)	90%	2.67×10^{-6}
rs10639111_TGAGA	NA	0.00 (–)	1%	2.68×10^{-6}
rs35144585_T	T / T	0.01 (↑)	89%	5.80×10^{-6}
rs73817091_T	NA	0.01 (–)	3%	1.94×10^{-5}
rs11383197_AG	GG / GG	0.00 (–)	75%	6.46×10^{-5}
rs2059639_C	C / C	0.00 (↑)	53%	7.64×10^{-5}

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.